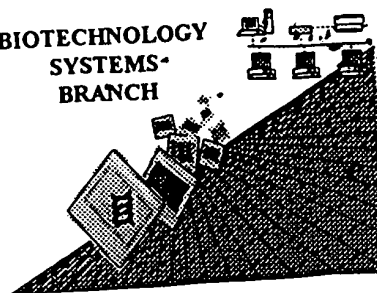


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS-
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/936921
Source: PCT 09
Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/936921

ERROR DETECTED

SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/936,921

DATE: 10/04/2001
 TIME: 10:50:38

Input Set : A:\seqlisting110530_pac.txt
 Output Set: N:\CRF3\10042001\I936921.raw

3 <110> APPLICANT: RAOULT, Didier
 4 LA SCOLA, Bernard
 5 BIRG, Marie-Laure
 6 FENOLLAR, Florence
 8 <120> TITLE OF INVENTION: Diagnosis of Whipple's Disease
 10 <130> FILE REFERENCE: 110530
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/936,921
 C--> 12 <141> CURRENT FILING DATE: 2001-09-20
 12 <150> PRIOR APPLICATION NUMBER: PCT/FR00/00754
 13 <151> PRIOR FILING DATE: 2000-03-24
 15 <150> PRIOR APPLICATION NUMBER: FR99/06679
 16 <151> PRIOR FILING DATE: 1999-05-21
 18 <150> PRIOR APPLICATION NUMBER: FR99/03989
 19 <151> PRIOR FILING DATE: 1999-03-26
 21 <160> NUMBER OF SEQ ID NOS: 5
 23 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 19
 27 <212> TYPE: DNA
 C--> 28 <213> ORGANISM: Artificial
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: primer
 33 <220> FEATURE:
 34 <221> NAME/KEY: modified_base
 35 <222> LOCATION: (2)..(2)
 36 <223> OTHER INFORMATION: i
 39 <220> FEATURE:
 40 <221> NAME/KEY: modified_base
 41 <222> LOCATION: (8)..(9)
 42 <223> OTHER INFORMATION: i
 45 <220> FEATURE:
 46 <221> NAME/KEY: modified_base
 47 <222> LOCATION: (11)..(11)
 48 <223> OTHER INFORMATION: i
 51 <400> SEQUENCE: 1
 W--> 52 ~~tnatgggnc naanatgca~~
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 20
 57 <212> TYPE: DNA
 C--> 58 <213> ORGANISM: Artificial
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: primer
 63 <220> FEATURE:
 64 <221> NAME/KEY: modified_base
 65 <222> LOCATION: (6)..(6)
 66 <223> OTHER INFORMATION: i
 69 <220> FEATURE:

Does Not Comply
 Corrected Diskette Needed

See page 1 of 4
 And Error Summary Sheet
 item nine.

Errored: location 14 in the sequence
 represented as an unknown is not
 identified in field 221, 222 or 223.

The type of errors shown ^{may} exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

19

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/936,921

DATE: 10/04/2001
 TIME: 10:50:38

Input Set : A:\seqlisting110530_pac.txt
 Output Set: N:\CRF3\10042001\I936921.raw

```

70 <221> NAME/KEY: modified_base
71 <222> LOCATION: (15)..(15)
72 <223> OTHER INFORMATION: i
75 <220> FEATURE:
76 <221> NAME/KEY: modified_base
77 <222> LOCATION: (18)..(18)
78 <223> OTHER INFORMATION: i
81 <400> SEQUENCE: 20
W--> 82 gcccancatt ccatntcncc
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 612
87 <212> TYPE: DNA
88 <213> ORGANISM: Tropheryma whippelii
90 <220> FEATURE:
91 <221> NAME/KEY: misc_feature
92 <222> LOCATION: (1)..(612) 0-V
93 <223> OTHER INFORMATION: n=a or g or c or t/u, unknown, or other.
96 <400> SEQUENCE: 3
W--> 97 aagtccccng gacgganag gnatggagng gtatgtancg atcgatgcgg gtgatgtttt 60
W--> 99 aattgccnag gatccgggca ttgtggggga tgtttccgct gatgttgta ctgtcannca 120
101 ggatgacggg aaacatcgcg actaccatgt tggtaaattt gttcgttcaa atcagggcaa 180
W--> 103 ctgtttacaac cagcnagtgt tgggtccgatc cggagatcgt gtataaaaag gtacagttct 240
105 tgcacatggt ccatgtactg acaaagggtga gcttagtctt ggtagaaatc ttctggttgc 300
107 tttcatgccc tgggagggct ataactttga ggatgcgata attatcagcc agaatttggt 360
W--> 109 caaggacgac accctttcnt caatccacat agaagaacat gaggttagca cccgggatac 420
W--> 111 gaagctgggc agtganagaa ataacgcgag accttccgaa tgtaagcatg gattacataa 480
113 aggacttgga cgaacggggt attatccgga ttggcgctga ggttgccctt ggggacattt 540
115 tggttggtaa ggtgacccca aagggcgaa accgaactca acgcggaaga acgtttgctg 600
117 agggctatct tt 612
120 <210> SEQ ID NO: 4
121 <211> LENGTH: 18
122 <212> TYPE: DNA
C--> 123 <213> ORGANISM: Artificial
125 <220> FEATURE:
126 <223> OTHER INFORMATION: oligonucleotide
128 <400> SEQUENCE: 4 18
129 gcattgtggg ggatgttt
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 18
134 <212> TYPE: DNA
C--> 135 <213> ORGANISM: Artificial
137 <220> FEATURE:
138 <223> OTHER INFORMATION: oligonucleotide
140 <400> SEQUENCE: 5 18
141 ttgggggtcac cttaccaa

```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/936,921

DATE: 10/04/2001
TIME: 10:50:39

Input Set : A:\seqlisting110530_pac.txt
Output Set: N:\CRF3\10042001\I936921.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:58 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:123 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:135 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5